

Form 1449 (Modified)

**Information Disclosure  
Statement By Applicant**

(Use Several Sheets if Necessary)

Atty Docket No.

MXGNP002X1/0159.210US

Application No.:

09/495,668

Applicant:

Selifonov et al.

Filing Date

February 1, 2000

Group

1637




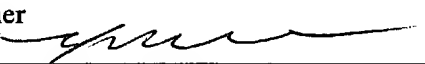
**U.S. Patent Documents**

Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
	A1						
	A2						
	A3						
	A4						
	A5						
	A6						
	A7						
	A8						

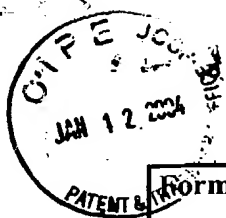
**Foreign Patent or Published Foreign Patent Application**

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation	
							Yes	No
	B1							
	B2							
	B3							
	B4							
	B5							

**Other Documents**

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	CS 262, Computational Genomics, Handout #1: Course Information, printed from: <a href="http://www.stanford.edu/class/cs">http://www.stanford.edu/class/cs</a> , Spring 2003, 11 pages
	C2	Corpet et al., Browsing Protein Families Via the Rich Family Description Format," Bioinformatics, Vol. 15, No. 12, 1999, Pages 1020-1027
	C3	Mironov et al., "Computer Analysis of Transcription Regulatory Patterns in Completely Sequenced Bacterial Genomes," Nucleic Acids Research, Vol. 27, No. 14, 1999, Pages 2981-2989
Examiner 		Date Considered 5-5-04

Examiner Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.



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**Other Documents**

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Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Aita et al., "Analysis of Local Fitness Landscape with a Model of the Rough Mt. Fuji-Type Landscape: Application to Prolyl Endopeptidase and Thermolysin," Biopolymers. Vol. 54, pp. 64-79, Accepted January 14, 2000
	C2	Hellberg et al., "The Prediction of Bradykinin Potentiating Potency of Pentapeptides. An Example of a Peptide Quantitative Structure-Activity Relationship," Acta Chemica Scandinavica B 40, pp. 135-140, 1988
	C3	Bucht et al., "Optimising the Signal Peptide for Glycosyl Phosphatidylinositol Modification of Human Acetylcholinesterase Using Mutational Analysis and Peptide-Quantitative Structure-Activity Relationships," Biochimica et Biophysica Acta 1431, pp. 471-482, 1999
	C4	Sandberg et al., "Engineering Multiple Properties of a Protein by Combinatorial Mutagenesis," Proc. Natl. Acad. Sci. USA, Vol. 90, pp. 8367-8371, September 1993
	C5	Wrede et al., "Peptide Design Aided by Neural Networks: Biological Activity of Artificial Signal Peptidase I Cleavage Sites," Biochemistry, 37, pp. 3588-3593, 1998
	C6	Jill Damborsky, "Quantitative Structure-Function and Structure-Stability Relationships of Purposely Modified Proteins," Protein Engineering, Vol. 11, no. 1, pp. 21-30, 1998
	C7	Hellberg, et al., "Peptide Quantitative Structure-Activity Relationships, a Multivariate Approach," J. Med Chem, 30: pp 1126-1195, 1987
	C8	Sandberg et al., "New Chemical Descriptors Relevant for the Design of Biologically Active Peptides. A Multivariate Characterization of 87 Amino Acids," J. Med Chem., 41, pp. 2481-2491, 1998
	C9	Casari et al., "A Method to Predict Functional Residues in Proteins," Nat. Struct Biol., 2, pp. 171-178, 1995
	C10	Gogos et al., "Assignment of Enzyme Substrate Specificity by Principal Component Analysis of Aligned Protein Sequences: An Experimental Test Using DNA Glycosylase Homologs," Proteins: Structure, Function, and Genetics, 40, pp. 98-105, 2000
	C11	Suzuki et al., "A Method for Detecting Positive Selection at Single Amino Acid Sites," Mol. Biol. Evol. 16 (10): pp. 1315-1328, 1999
	C12	Benner et al., "Amino Acid Substitution During Functionally Constrained Divergent Evolution of Protein Sequences," Protein Engineering, Vol. 7, No. 11, pp. 1323-1332, 1994

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<i>[Signature]</i>	C13	Wu et al., "Discovering Empirically Conserved Amino Acid Substitution Groups in Databases of Protein Families," Proc. Int. Conf. Intell. Syst. Mol. Biol., 4, pp. 230-240, 1996
<i>[Signature]</i>	C14	Adenot et al., "Peptides Quantitative Structure-Function Relationships: An Automated Mutation Strategy to Design Peptides and Pseudopeptides from Substitution Matrices," Journal of Molecular Graphics and Modelling, 17, pp. 292-309, 1999
<i>[Signature]</i>	C15	Norinder et al., "A Quantitative Structure-Activity Relationship Study of Some Substance P-Related Peptides," J. Peptide Res., 49, pp. 155-162, 1997
<i>[Signature]</i>	C16	Sandberg, "Deciphering Sequence Data a Multivariate Approach," Ph.D Thesis, Umea: Umea University, 78 pages, 1997
<i>[Signature]</i>	C17	Eriksson et al., "Peptide QSAR on Substance P Analogues, Enkephalins and Bradykinins Containing L-and D-Amino Acids," Acta Chemica Scandinavica, 44, pp. 50-56, 1990
<i>[Signature]</i>	C18	Ufkes et al., "Further Studies on the Structure-Activity Relationships of Bradykinin-Potentiating Peptides," European Journal of Pharmacology, 79, pp. 155-158, 1982
<i>[Signature]</i>	C19	Dobrynin et al., "Synthesis of Model Promoter for Gene Expression in Escherichia Coli," Symposium Series No. 7, pp. 365-376, 1980
<i>[Signature]</i>	C20	Skinner et al., "Potential Use of Additivity of Mutational Effects in Simplifying Protein Engineering," Proc. Natl. Acad. Sci., Vol. 93, pp. 10753-10757, 1996
<i>[Signature]</i>	C21	Aita et al., "Theory of Evolutionary Molecular Engineering Through Simultaneous Accumulation of Advantageous Mutations," J. Theor. Biol., 207, pp/ 543-556, 2000
<i>[Signature]</i>	C22	Lathrop et al., "Global Optimum Protein Threading with Gapped Alignment and Empirical Pair Score Functions," J. Mol. Biol., 255, pp. 641-665, 1996
<i>[Signature]</i>	C23	Hellberg et al., "A Multivariate Approach to QSAR," Ph.D. Thesis, Umea, Sweden: University of Umea: 1986
<i>[Signature]</i>	C24	"Vector NTI Suite 7.0 User's Manual (portion) describing software believed to be available prior to February 1, 2000
Examiner <i>[Signature]</i>	Date Considered 5-5-04	

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